

1 CAAACTTGGT GGCAACTTGC CTCCCGGTGC GGGCGTCTCT CCCCCACCGT
51 CTCAA CATGC TTAGGGGTCC GGGGCCCGGG CTGCTGCTGC TGGCCGTCCA
101 GTGCCTGGGG ACAGCGGTGC CCTCCACGGG AGCCTCGAAG AGCAAGAGGC
151 AGGCTCAGCA AATGGTTCAG CCCCACTCCC CGGTGGCTGT CAGTCAAAGC
201 AAGCCCGGTT GTTATGACAA TGGAAACAC TATCAGATAA ATCAACAGTG
251 GGAGCGGACC TACCTAGGCA ATGCGTTGGT TTGTACTTGT TATGGAGGAA
301 GCCGAGGTTT TAACTGCGAG AGTAAACCTG AAGCTGAAGA GACTTGCTTT
351 GACAAGTACA CTGGGAACAC TTACCGAGTG GGTGACACTT ATGAGCGTCC
401 TAAAGACTCC ATGATCTGGG ACTGTACCTG CATCGGGGCT GGGCGAGGGA
451 GAATAAGCTG TACCATCGCA AACCGCTGCC ATGAAGGGGG TCAGTCCTAC
501 AAGATTGGTG ACACCTGGAG GAGACCACAT GAGACTGGTG GTTACATGTT
551 AGAGTGTGTG TGICTTGGTA ATGGAAAAGG AGAATGGACC TGCAAGCCCA
601 TAGCTGAGAA GTGTTTTGAT CATGCTGCTG GGACTTCCTA TGTGGTCGGA
651 GAAACGTGGG AGAAGCCCTA CCAAGGCTGG ATGATGGTAG ATTGTACTTG
701 CCTGGGAGAA GGCAGCGGAC GCATCACTTG CACTTCTAGA AATAGATGCA
751 ACGATCAGGA CACAAGGACA TCCTATAGAA TTGGAGACAC CTGGAGCAAG
801 AAGGATAATC GAGGAAACCT GCTCCAGTGC ATCTGCACAG GCAACGGCCG
851 AGGAGAGTGG AAGTGTGAGA GGCACACCTC TGTGCAGACC ACATCGAGCG
901 GATCTGCCCC CTTCAACGAT GTTCGTGCAG CTGTTTACCA ACCGCGACCT
951 CACCCCCAGC CTCCTCCCTA TGGCCACTGT GTCACAGACA GTGGTGTGGT
1001 CTACTCTGTG GGGATGCAGT GGCTGAAGAC ACAAGGAAAT AAGCAAAATG
1051 TTTGCACGTG CCTGGGCAAC GGAGTCAGCT GCCAAGAGAC AGCTGTAACC

Fig. 1 (part 1)

1101 CAGACTTACG GTGGCAACTC AATGGAGAG CCATGTGTCT TACCATTAC
1151 CTACAACGAC AGGACGGACA GCACAACTTC GAATTATGAG CAGGACCAGA
1201 AATACTCTTT CTGCACAGAC CACACTGTTT TGGTTCAGAC TCGAGGAGGA
1251 AATTCCAATG GTGCCTTG TG CCACTTCCCC TTCCTATACA ACAACCACAA
1301 TTACACTGAT TGCACCTCTG AGGGCAGAAG AGACAACATG AAGTGGTGTG
1351 GGACCACACA GAACTATGAT GCCGACCAGA AGTTTGGGTT CTGCCCCATG
1401 GCTGCCACG AGGAAATCTG CACAACCAAT GAAGGGGTCA TGTACCGCAT
1451 TGGAGATCAG TGGGATAAGC AGCATGACAT GGGTCACATG ATGAGGTGCA
1501 CGTGTGTG TG GAATGGTCGT GGGGAATGGA CATGCATTGC CTACTCGCAG
1551 CTTGAGATC AGTGCATTGT TGATGACATC ACTTACAATG TGAACGACAC
1601 ATTCCACAAG CGTCATGAAG AGGGGCACAT GCTGAACTGT ACATGCTTCG
1651 GTCAGGGTCG GGGCAGGTGG AAGTGTGATC CCGTCGACCA ATGCCAGGAT
1701 TCAGAGACTG GGACGTTTTA TCAAATTGGA GATTTCATGG AGAAGTATGT
1751 GCATGGTGTC AGATACCAGT GCTACTGCTA TGGCCGTGGC ATTGGGGAGT
1801 GGCATTGCCA ACCTTTACAG ACCTATCCAA GCTCAAGTGG TCCTGTCGAA
1851 GTATTATCA CTGAGACTCC GAGTCAGCCC AACTCCCACC CCATCCAGTG
1901 GAATGCACCA CAGCCATCTC ACATTTCCAA GTACATTCTC AGGTGGAGAC
1951 CTGTGAGTAT CCCACCCAGA AACCTTGGAT ACTGAGTCTC CTAATCTTAT
2001 CAATTCTGAT GGTTCCTTT TTTCCAGCT TTTGAGCCAA CAACTCTGAT
2051 TAACTATTCC TATAGCATTT ACTATATTTG TTTAGTGAAC AAACAATATG
2101 TGGTCAATTA AATTGACTTG TAGACTGAAA AAAAAAAAAA AAAAAA

Fig. 1 (part 2)

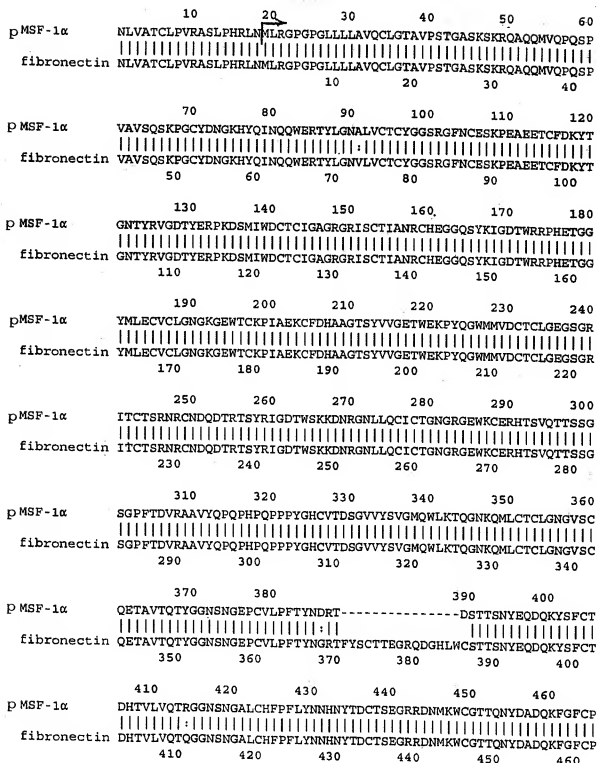


Fig. 2 (part 1)

	470	480	490	500	510	520
pMSF-1α	MAAHEEICTTNEGVMYRIGDQWDKQHDGMHMRCTCVGNRGGEWTCIAYSQLRDQCIVDD					
fibronectin	MAAHEEICTTNEGVMYRIGDQWDKQHDGMHMRCTCVGNRGGEWTCIAYSQLRDQCIVDD					
	470	480	490	500	510	520
	530	540	550	560	570	580
pMSF-1α	ITYNVNDTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTFTFYQIGDSWEKYVHG					
fibronectin	ITYNVNDTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTFTFYQIGDSWEKYVHG					
	530	540	550	560	570	580
	590	600	610	620	630	640
pMSF-1α	VRYQCYCYGRGIGEWHCQPLQTYPSSSGPVEVFITETPSQPNSHPIQWNAQPQSHISKYI					
fibronectin	VRYQCYCYGRGIGEWHCQPLQTYPSSSGPVEVFITETPSQPNSHPIQWNAQPQSHISKYI					
	590	600	610	620	630	640
	650	660	670	680	690	700
pMSF-1α	LRWRPVSIPPRLGYKVSXSQFXWFLFFPAFETTLINYSYSIIYICLVNKKQYVNVXID					
	: →					
	(SEQ IS NO.: 18)					
fibronectin	LRWRPKNSVGRWKEATIPGHLNSYTIKGLKPGVVYEGQLISIQYQGHQEVTRPFDFTTST					
	650	660	670	680	690	700

(SEQ IS NO.: 17)

Fig. 2 (part 2)

SEQ ID NO:	Sequence Type	Binding Site
1NVAATCLEVPAASLEPHRLN	[SEQ ID NO: 13]	5' untranslated region
14LNGPSPGILLAVOCIGTAVPSTGASKSR	[SEQ ID NO: 14]	Signal
22QAOQMOVOPSPFVAVSQSKFQ	[SEQ ID NO: 15]	NH ₂ -terminal segment
32CYDNKGKHYOINQOMERTYLGNALVCTCYGSSRGFNCSEKPEAEET	[SEQ ID NO: 16]	I
37CDEKTYTGNTRYRGDTEREPDSDMIDCTCIGARGKISCTIAAR	[SEQ ID NO: 38]	I
144CHEGGQSKYIGDTRRPHETGTMLEVCIGNGKGEWTCPIAEK	[SEQ ID NO: 39]	I
184QEPHAGSYVGEITWEKYGQMMWVDCICGSSGHLTGTSRNR	[SEQ ID NO: 40]	I
22QANDQDTKTRIDTWSKDRGNLLQICITGNGRGEMKCR	[SEQ ID NO: 17]	I
27HRSVQTTSSSGSGETVDVAAYQPFQHPPEPYGH	[SEQ ID NO: 18]	Connecting strand
305CVTDGTVVYVSGMQLKTQGNKQMLCTCLGNGVSCQE	[SEQ ID NO: 19]	I
348PAVITQYVGSNSNEPCVLFTYNDRTDSTTSNYEODOKYSFCTDH	[SEQ ID NO: 20]	II
390VLYVOTGSGNSGALCHPEFLYNNHNYTDCISEGRDNKMGCGTT	[SEQ ID NO: 28]	II
ONKIDADKQGFQPMALHELI		Gelatin
455CTTNEGTVHAGIDQMDKOHMGHMRCTVGNRGEMTCIAVSQLRQD	[SEQ ID NO: 21]	I
503CTVDDITTYNNDPFRKRESGHMLNCTQGGGRRGKMDPDQD	[SEQ ID NO: 22]	I
545QDSDSTGTFYQDGDMEXYHGVRYCYCYGRGIGEMHQCFLOTYBS	[SEQ ID NO: 23]	I
594SGEVEVETITETPSQNSHPQANAPQPSHISKYILMRP	[SEQ ID NO: 24]	III
63N/SIDPRNLGY	[SEQ ID NO: 25]	Unique Sequence
*V8*SYQ*MELEFFPAFETTLINYSYSIYICLVNRQYVN*IDL*TEKKKKK[SEQ ID NO: 29-33]3' untranslated region		

Figure 3

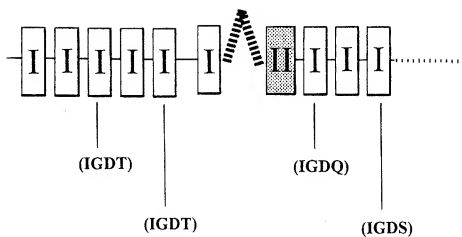


Fig. 4

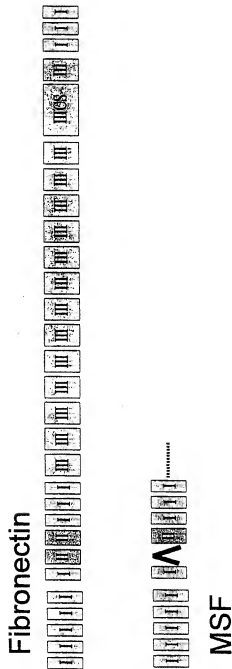


Fig. 5